

1/23

GCTCTCCCTGCTCCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTG
M R A L E G P G L S L L
TGCCTGGTGTGGCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAA
C L V L A L P A L L P V P A V R G V A E
ACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGC
T P T Y P W R D A E T G E R L V C A Q C
CCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCG
P P G T F V Q R P C R R D S P T T C G P
TGTCCACCGCGCCACTACACGCAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAAC
C P P R H Y T Q F W N Y L E R C R Y C N
GTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCC
V L C G E R E E E A R A C H A T H N R A
TGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGT
C R C R T G F F A H A G F C L E H A S C
CCACCTGGTGCCGGCGTGATTGCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCG
P P G A G V I A P G T P S Q N T Q C Q P
TGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGC
C P P G T F S A S S S S S E Q C Q P H R
AACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTG
N C T A L G L A L N V P G S S S H D T L
TGCACAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
C T S C T G F P L S T R V P G A E E C E
CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTG
R A V I D F V A F Q D I S I K R L Q R L
CTGCAGGCCCTCGAGGCCCGGAGGGCTGGGCTCCGACACCAAGGGCGGGCGCGCGCC
L Q A L E A P E G W G P T P R A G R A A
TTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTG
L Q L K L R R R L T E L L G A Q D G A L
CTGGTGCGGCTGCTGCAGGCGCTGCGCGTGCCAGGATGCCCGGGCTGGAGCGGAGCGTC
L V R L L Q A L R V A R M P G L E R S V
CGTGAGCGCTTCTCCCTGTGCACTGATCCTGGCCCCCTTATTTATTCTACATCCTTG
R E R F L P V H *
GCACCCCACTTGCACTGAAAGAGGCTTTTTTTTAAATAGAAGAAATGAGGTTTCTTAAAG
CTTATTTTTATAAAGCTTTTTTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG.1

2/23

TGGCATGTGGTCAGGCACAGCAGGGTCTGTGTCCGCGCTGAGCCGCGCTCTCCCTGCT
CCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTGTGCCTGGTGTG
M R A L E G P G L S L L C L V L
GCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTAC
A L P A L L P V P A V R G V A E T P T Y
CCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCCCCCAGGCACC
P W R D A E T G E R L V C A Q C P P G T
TTTGTGCAGCGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGC
F V Q R P C R R D S P T T C G P C P P R
CACTACACGCAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGG
H Y T Q F W N Y L E R C R Y C N V L C G
GAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGC
E R E E E A R A C H A T H N R A C R C R
ACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCC
T G F F A H A G F C L E H A S C P P G A
GGCGTGATTGCCCCGGGTGAGAGCTGGGCGAGGGGAGGGGCCCCAGGAGTGGTGGCCGG
G V I A P G E S W A R G G A P R S G G R
AGGTGTGGCAGGGGTGAGTTGCTGGTCCCAGCCTTGACCCCTGAGCTAGGACACCAATT
R C G R G Q V A G P S L A P *
CCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCAGAACACGCAGTGCCA
GCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCA
CCGCAACTGCACGGCCCTGGGCTGGCCCTCAATGTGCCAGGCTCTTCCCTCCCATGACAC
CCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCAGAGGC
CTGAGGGGGCAGCACACTGCAGGCCAGGCCCACTTGTGCCCTCACTCCTGCCCCCTGCACG
TGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGGAAGGGGCCACAGTGGATTTGAGGGG
TCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGCCCTCTCAGGGGTGGCTGAGAATTT
GGATCTGAGCCAGGGCACAGCCTCCCCTGGAGAGCTCTGGGAAAGTGGGCAGCAATCTCC

FIG.2A

3/23

TAAC TGCCCGAGGGGAAGGTGGCTGGCTCCTCTGACACGGGGAAACCGAGGCCTGATGGT
AACTCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCTCTGACATGGGGAAACCGAGGC
CCAATGTTAACCCTGTTGAGAAGTCACAGGGGGAAGTGACCCCTTAACATCAAGTCAG
GTCCGGTCCATCTGCAGGTCCCAACTCGCCCCTTCGATGGCCAGGAGCCCCAAGCCCT
TGCCTGGGCCCCCTTGCTCTTGACGCCAAGGTCCGAGTGGCCGCTCCTGCCCCCTAGGC
CTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCCTTCTCCAGTCCCCATCGTTGCACT
GCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTCTCCTGCAAACCCCCGAGTGG
GGCCAGAAAGCAGGGTACCTGGCAGCCCCCGCCAGTGTGTGTGGGTGAAATGATCGGAC
CGCTGCCTCCCCACCCCACTGCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTG
TGGCTTTCCAGGACATCTCCATCAAGAGGAGCGGCTGCTGCAGGCCC

FIG.2B

1	M	-	G	L	S	T	V	P	D	L	L	P	L	V	L	E	L	V	G	I	Y	P	S	G	V	I	G	L	V	P	H	L	G	D	R	E	-	TNFR1	
1	M	A	P	V	A	V	W	A	A	L	A	V	G	L	E	L	W	A	A	H	A	L	P	A	Q	V	A	-	-	-	-	-	F	T	P	-	-	TNFR2	
1	M	G	A	G	A	T	G	R	A	M	D	-	-	-	G	P	R	L	L	L	L	L	G	V	S	L	G	G	A	K	E	-	A	C	P	-	-	NGFR	
1	M	-	R	L	P	R	-	A	S	S	P	C	G	L	A	W	G	P	L	L	L	G	L	V	A	S	Q	P	Q	L	V	P	P	-	-	-	LT6R		
1	M	L	G	I	W	T	-	-	-	L	P	L	V	L	T	S	V	-	A	R	L	S	S	K	S	V	N	A	Q	V	T	D	I	N	S	K	G	L	FAS
1	M	-	-	-	-	A	R	P	H	P	-	-	-	-	W	W	L	C	V	L	G	T	L	V	G	L	S	-	A	T	P	A	P	K	S	C	P	-	CD27
1	M	R	V	L	-	-	-	-	-	-	-	-	-	-	L	A	A	L	G	L	L	F	L	G	A	L	R	A	-	-	-	-	F	P	Q	-	-	CD30	
1	M	V	R	L	P	L	-	Q	-	-	-	C	V	L	-	W	G	C	L	L	-	-	-	-	T	A	V	H	P	E	-	-	P	P	-	-	CD40		
1	M	G	N	-	-	-	-	-	-	S	C	Y	N	I	V	A	T	L	L	L	V	L	N	-	-	-	-	-	-	-	-	F	E	R	-	-	4-1BB		
1	M	C	V	G	A	-	-	R	R	L	G	-	-	-	R	G	P	C	A	A	L	L	L	G	L	G	L	S	T	V	T	G	L	H	C	V	-	-	OX40
1	M	K	S	V	-	L	Y	L	I	-	-	-	L	F	L	S	C	I	I	I	N	G	R	D	A	P	-	-	-	-	-	Y	T	P	-	-	VC22		
1	M	K	S	-	-	-	Y	I	L	L	-	-	L	L	L	S	C	I	I	I	I	N	S	D	I	T	P	-	-	-	-	H	E	P	-	-	CRMB		
1	M	R	A	L	E	-	-	-	-	-	G	P	G	L	S	L	L	C	L	V	L	A	L	P	A	L	L	P	-	-	-	-	V	P	A	-	-	TNFR-6a	
1	M	R	A	L	E	-	-	-	-	-	-	G	P	G	L	S	L	L	C	L	V	L	A	L	P	A	L	L	P	-	-	-	-	V	P	A	-	-	TNFR-6b

FIG.3A

39	-	-	K	R	D	S	V	C	P	Q	G	K	Y	I	H	-	-	P	Q	N	S	I	C	C	T	K	C	H	K	G	T	Y	L	Y	N	D	C	P	G	TNFR1		
32	-	-	Y	-	A	P	E	P	G	S	T	C	R	L	R	E	Y	Y	D	Q	T	A	Q	M	C	C	S	K	C	S	P	G	Q	H	A	K	V	F	C	-	TNFR2	
34	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	G	L	Y	T	H	S	G	E	-	C	C	K	A	C	N	L	G	E	G	V	A	Q	P	C	G	A	NGFR
36	-	-	Y	R	I	E	N	Q	T	C	W	D	Q	D	K	E	Y	Y	E	P	M	H	D	V	C	C	S	R	C	P	P	G	E	F	V	F	A	V	C	-	Lt6R	
36	E	L	R	K	T	V	T	T	T	V	E	T	Q	N	L	E	G	L	H	H	D	G	Q	F	C	H	K	P	C	P	P	G	E	R	K	A	R	D	C	T	V	FAS
29	-	E	-	-	-	-	-	-	-	-	-	-	-	-	-	R	H	Y	W	A	Q	G	K	L	C	C	Q	M	C	E	P	G	T	F	L	V	K	D	C	D	Q	CD27
22	-	D	R	P	F	E	D	T	C	H	G	N	P	S	H	Y	Y	D	K	A	V	R	R	C	C	C	Y	R	C	P	M	G	L	F	P	T	Q	Q	C	P	Q	CD30
24	-	-	-	-	-	T	A	C	R	E	-	-	-	-	-	K	Q	Y	L	-	I	N	S	Q	-	C	C	S	L	C	Q	P	G	Q	K	L	V	S	D	C	-	CD40
21	-	T	R	S	L	Q	D	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	C	S	N	C	P	A	G	T	F	-	-	-	C	D	N	4-1BB
33	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	D	T	Y	P	S	N	D	R	-	C	C	H	E	C	R	P	G	N	G	M	V	S	R	C	S	R	OX40
28	-	P	N	G	K	C	K	D	T	E	Y	K	R	H	N	-	-	-	-	-	-	-	L	C	C	L	S	C	P	P	G	T	Y	A	S	R	L	C	D	S	VC22	
26	-	S	N	G	K	C	K	D	N	E	Y	K	R	H	H	-	-	-	-	-	-	-	L	C	C	L	S	C	P	P	G	T	Y	A	S	R	L	C	D	S	CRMB	
27	-	V	R	G	V	A	E	T	P	T	Y	P	W	R	D	A	-	E	T	G	E	R	L	V	C	A	Q	C	P	P	G	T	F	V	Q	R	P	C	-	-	TNFR-6a	
27	-	V	R	G	V	A	E	T	P	T	Y	P	W	R	D	A	-	E	T	G	E	R	L	V	C	A	Q	C	P	P	G	T	F	V	Q	R	P	C	-	-	TNFR-6b	

FIG.3B

75	P	-	G	Q	D	T	D	C	R	-	E	C	-	E	S	G	S	-	F	T	A	S	E	N	H	L	R	H	C	L	S	C	S	K	-	C	R	K	E	M	G	TNFR1	
68	T	K	T	S	D	T	V	C	-	D	S	C	-	E	D	S	T	Y	T	Q	L	W	N	W	V	P	E	C	L	S	C	G	S	R	-	C	S	D	Q	V	TNFR2		
60	N	Q	-	T	-	V	-	C	E	-	P	C	-	L	D	S	V	T	F	S	D	V	V	S	A	T	E	P	C	K	P	C	T	-	E	C	V	G	L	Q	S	NGFR	
73	S	R	S	Q	D	T	V	C	-	K	T	C	-	Q	P	H	N	S	Y	N	E	H	W	N	H	L	S	T	C	Q	L	C	R	P	-	C	D	I	V	L	G	LTbR	
76	H	-	G	D	E	P	D	C	V	-	P	C	-	E	G	K	E	Y	T	D	K	A	H	F	S	S	K	-	C	R	R	C	R	L	-	C	D	E	G	H	G	FAS	
56	H	R	K	A	-	A	Q	C	D	-	P	C	-	I	P	G	V	S	F	S	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CD27	
61	R	-	-	-	P	T	D	C	R	K	Q	C	-	E	P	D	Y	Y	L	D	E	A	D	R	C	T	A	C	V	T	C	S	-	-	-	R	D	D	D	CD30			
52	T	E	F	T	E	T	E	C	-	L	P	C	-	-	G	E	S	E	F	L	D	T	W	N	R	E	T	H	C	H	Q	H	K	Y	-	C	D	P	N	L	G	CD40	
40	N	R	N	Q	-	-	I	C	-	S	P	C	-	-	P	P	N	S	F	S	S	A	-	G	G	Q	R	T	C	D	I	C	R	-	Q	-	-	-	-	K	G	4-1BB	
59	S	Q	N	T	-	V	-	C	R	-	P	C	-	-	G	P	G	F	Y	N	D	V	V	S	S	K	-	P	C	K	P	C	T	-	W	C	-	N	L	R	S	OX40	
60	K	T	N	T	-	-	Q	C	-	T	P	C	-	G	S	G	T	F	T	G	R	N	N	H	L	P	A	C	L	S	C	N	G	R	-	C	N	S	N	Q	V	VC22	
58	K	T	N	T	N	T	Q	C	-	T	P	C	-	-	A	S	D	T	F	T	S	R	N	N	H	L	P	A	C	L	S	C	N	G	R	-	C	D	S	N	Q	V	CRMB
63	R	R	D	S	P	T	T	C	-	G	P	C	-	P	P	R	H	Y	T	Q	F	W	N	Y	L	E	R	C	R	Y	C	N	V	L	C	G	E	R	E	E	E	TNFR-6a	
63	R	R	D	S	P	T	T	C	-	G	P	C	-	P	P	R	H	Y	T	Q	F	W	N	Y	L	E	R	C	R	Y	C	N	V	L	C	G	E	R	E	E	E	TNFR-6b	

FIG.3C

111	-	Q	V	E	I	S	C	T	V	D	R	D	T	V	C	G	C	R	K	N	Q	Y	R	H	Y	W	S	E	N	L	F	Q	C	F	N	C	S	L	-	TNFR1	
106	-	-	-	E	T	Q	A	-	C	T	R	E	Q	N	R	I	C	T	C	R	P	G	W	Y	C	A	L	S	K	Q	E	-	G	C	R	L	C	A	P	L	TNFR2
95	M	S	A	P	-	-	-	-	C	V	E	A	D	D	A	V	C	R	C	A	Y	G	Y	-	Q	D	E	T	T	G	-	R	C	E	A	C	R	V	-	NGFR	
110	F	E	E	V	A	P	-	C	T	S	D	R	K	A	E	C	R	C	Q	P	G	M	S	C	V	Y	L	D	N	E	-	-	C	V	H	C	E	E	L	TbR	
113	L	E	V	E	I	N	-	C	T	R	T	Q	N	T	K	C	R	C	K	P	N	-	-	-	-	-	-	-	-	-	-	-	-	-	F	F	C	N	-	-	FAS
74	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D	H	H	T	R	P	-	-	H	C	E	S	C	R	H	-	CD27		
92	L	V	E	K	T	P	-	C	A	W	N	S	S	R	V	C	E	C	R	P	G	M	F	C	S	T	S	A	V	N	-	-	S	C	A	R	C	F	H	CD30	
89	L	R	V	Q	Q	K	-	G	T	S	E	T	D	T	I	C	T	C	E	E	G	W	H	C	T	-	-	S	E	A	-	-	-	C	E	S	C	V	L	H	CD40
71	V	F	R	T	R	K	E	C	S	S	T	S	H	A	E	C	D	C	T	P	G	F	H	C	L	-	-	G	A	-	-	G	C	S	M	C	E	Q	D	4-1BB	
92	G	S	E	R	K	Q	L	C	T	A	T	Q	D	T	V	C	R	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OX40	
96	-	-	E	T	R	S	-	C	N	T	T	H	H	R	I	C	E	C	S	P	G	Y	Y	C	L	L	K	G	S	-	-	G	C	K	A	C	V	S	Q	VC22	
96	-	-	E	T	R	S	-	C	N	T	T	H	N	R	I	C	D	C	A	P	G	Y	Y	C	F	L	K	G	S	-	-	G	C	K	A	C	V	S	Q	CRMB	
101	-	-	E	A	R	A	-	C	H	A	T	H	N	R	A	C	R	C	R	T	G	F	F	-	-	-	-	A	H	A	-	-	G	-	-	F	C	L	E	H	TNFR-6a
101	-	-	E	A	R	A	-	C	H	A	T	H	N	R	A	C	R	C	R	T	G	F	F	-	-	-	-	A	H	A	-	-	G	-	-	F	C	L	E	H	TNFR-6b

FIG.3D

149	-	-	-	-	C	L	N	G	T	V	H	L	-	-	S	C	Q	E	K	Q	N	T	V	C	T	-	C	H	A	G	F	F	L	R	E	-	-	-	N	TNFR1		
141	R	-	-	-	K	C	R	P	G	F	G	V	A	R	P	G	T	E	T	S	D	V	V	-	C	K	P	C	A	P	G	T	F	S	N	T	S	S	T	D	TNFR2	
128	-	-	-	-	-	C	E	A	G	S	G	L	V	-	F	S	C	Q	D	K	Q	N	T	V	C	E	E	C	P	D	G	T	Y	S	D	E	A	N	H	V	D	NGFR
146	R	L	V	L	-	C	Q	P	G	T	E	A	E	V	T	D	E	I	M	D	T	D	V	N	V	C	V	P	C	K	P	G	H	F	Q	N	T	S	P	R	A	LTbR
137	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	T	V	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	E	FAS	
87	-	-	-	-	-	C	H	S	G	L	-	L	V	-	R	N	C	T	I	T	A	N	A	E	C	A	-	C	R	N	G	W	-	-	-	-	-	-	-	-	-	CD27
129	S	V	-	-	-	C	P	A	G	M	I	V	K	F	P	G	T	A	Q	K	N	T	V	-	C	E	P	A	S	P	G	V	-	S	P	A	C	A	S	P	E	CD30
123	R	-	-	-	S	C	S	P	G	F	G	V	K	Q	I	A	T	G	V	S	D	T	I	-	C	E	P	C	P	V	G	F	F	S	N	V	S	S	A	F	E	CD40
106	-	-	-	-	-	C	K	Q	G	Q	E	L	T	K	K	G	-	-	-	-	-	-	-	-	C	K	D	C	C	F	G	T	F	N	D	Q	K	R	G	I	-	4-1BB
110	-	-	-	-	-	-	R	A	G	T	Q	P	L	-	D	S	Y	-	-	K	P	G	V	D	C	A	P	C	P	P	G	H	F	S	P	G	D	N	Q	-	-	OX40
131	T	-	-	-	K	C	G	I	G	Y	G	V	S	G	H	-	T	S	V	G	D	V	I	-	C	S	P	C	G	F	G	T	Y	S	H	T	V	S	S	A	D	VC22
131	T	-	-	-	K	C	G	I	G	Y	G	V	S	G	H	-	T	P	T	G	D	V	V	-	C	S	P	C	G	L	G	T	Y	S	H	T	V	S	S	V	D	CRMB
130	A	-	-	-	S	C	P	P	G	A	G	V	I	A	P	G	T	P	S	Q	N	T	Q	-	C	Q	P	C	P	P	G	T	F	S	A	S	S	S	S	E	TNFR-6a	
130	A	-	-	-	S	C	P	P	G	A	G	V	I	A	P	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6b	

FIG.3E

[illegible]

FIG. 3F

[illegible]

FIG. 3G

[illegible]

FIG. 3H

[illegible]

FIG. 31

264	T	K	P	L	A	P	N	P	S	F	S	P	T	P	G	F	T	P	T	L	G	F	S	P	V	P	S	S	T	F	T	S	S	S	T	Y	T	P	G	D	TNFR1	
294	-	-	-	-	-	-	L	Q	R	E	A	K	V	P	H	L	P	A	-	D	K	A	R	G	T	Q	G	P	E	Q	Q	H	L	L	I	T	A	-	-	TNFR2		
281	-	-	-	-	-	-	-	-	N	K	Q	G	A	N	S	R	P	P	V	-	N	Q	T	P	P	P	E	G	E	K	L	H	S	D	S	G	I	S	V	D	NGFR	
262	-	-	-	-	-	-	-	-	P	E	G	E	S	P	P	C	P	A	-	P	R	A	D	P	H	F	F	D	L	A	E	P	L	-	-	-	-	-	-	LIbR		
212	-	-	-	-	-	-	S	P	T	L	N	P	E	-	-	-	T	V	A	I	N	L	S	D	V	D	L	S	K	Y	I	T	-	-	-	-	-	-	-	FAS		
169	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L P CD27				
322	T	T	F	E	A	P	P	L	G	T	Q	P	D	C	N	P	T	P	E	-	N	G	E	A	P	A	S	T	S	P	T	Q	S	L	L	V	D	S	Q	A	CD30	
222	-	-	-	-	-	-	-	-	P	T	N	K	A	P	H	P	K	Q	E	-	P	Q	-	E	I	N	F	P	D	-	-	-	-	-	-	-	-	-	-	CD40		
193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4-1BB			
198	-	-	-	-	-	-	-	-	-	T	S	Q	G	P	S	T	R	P	V	-	E	-	-	-	V	P	G	G	R	A	V	A	A	I	L	G	L	G	L	-	OX40	
255	-	-	-	-	-	-	-	-	L	N	F	E	I	K	C	N	N	-	-	-	-	-	-	K	G	S	-	-	S	F	K	Q	-	-	-	L	T	K	-	-	VC22	
255	-	-	-	-	-	-	-	-	L	N	F	E	I	K	C	N	N	-	-	-	-	-	-	K	D	S	Y	S	S	S	K	Q	-	-	-	L	T	K	-	-	CRMB	
229	-	-	-	-	-	-	-	-	L	Q	R	L	L	Q	A	L	E	A	P	E	-	G	W	-	-	G	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6a
143	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	E	-	-	S	W	A	R	G	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6b

FIG.3J

[illegible]

FIG. 3G

[illegible]

FIG. 3K

329	-	-	-	-	L	A	S	D	P	I	P	N	P	L	Q	K	W	E	D	S	A	H	K	P	Q	S	L	D	T	D	D	P	A	T	L	Y	A	V	V	E	TNFR1	
339	-	-	-	-	-	-	-	-	-	D	R	R	A	P	T	R	N	Q	P	Q	A	P	G	V	E	A	S	G	A	G	E	A	R	A	S	T	G	S	S	S	TNFR2	
347	V	E	K	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	G	S	NGFR			
303	-	-	-	-	-	-	-	-	-	A	P	S	L	E	E	V	V	L	Q	Q	S	P	L	-	-	-	-	-	-	-	V	Q	A	R	E	L	-	-	E	A	E	LTbR
240	-	-	-	-	M	T	L	S	Q	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	FAS				
207	G	A	L	F	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	H	Q	-	CD27			
401	S	S	A	F	L	L	C	H	R	R	A	C	R	K	R	I	R	Q	K	L	H	L	C	Y	P	V	Q	T	S	Q	P	K	L	E	L	V	D	S	R	P	CD30	
252	-	-	-	-	-	-	-	-	Q	E	T	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CD40			
216	G	R	K	K	L	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4-1BB				
245	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OX40				
281	-	-	-	-	-	-	-	-	-	-	-	-	-	M	S	H	S	E	T	V	T	L	A	G	D	C	L	S	S	V	D	I	Y	I	L	Y	S	N	T	N	VC22	
284	-	-	-	-	-	-	-	-	-	-	-	-	-	M	P	H	S	E	S	V	T	L	V	G	D	C	L	S	S	V	D	I	Y	I	L	Y	S	N	T	N	CRMB	
258	-	-	-	-	-	-	-	-	R	R	R	L	T	E	L	L	G	A	Q	D	G	A	L	L	V	R	L	L	Q	A	L	R	-	-	-	-	-	-	-	-	TNFR-6a	
155	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6b				

FIG.3L

365	N	V	P	P	L	R	W	K	E	F	V	R	R	L	G	L	S	D	H	E	I	D	R	L	E	L	Q	N	G	R	C	L	R	E	A	Q	Y	S	M	L	TNFR1	
372	P	G	G	H	G	T	Q	V	N	V	T	C	I	V	N	V	C	S	S	D	H	-	S	S	Q	C	C	S	S	Q	A	S	S	T	M	G	D	T	-	-	TNFR2	
355	A	G	D	T	W	R	H	L	A	G	E	L	G	Y	Q	P	E	H	I	D	S	F	T	H	E	A	C	P	V	R	-	-	-	-	-	-	-	A	L	L	NGFR	
327	P	G	E	H	G	Q	V	A	H	G	A	N	G	I	H	V	T	G	S	V	T	V	T	G	N	I	Y	I	Y	N	G	P	V	L	G	G	T	-	-	LTbR		
246	-	-	-	-	-	-	-	-	K	G	F	V	R	K	N	G	V	N	E	A	K	I	D	E	I	K	N	D	N	V	Q	D	T	A	E	Q	K	V	Q	L	L	FAS
214	-	-	-	-	-	-	-	R	R	K	Y	R	S	N	K	G	E	S	P	V	E	P	A	E	P	C	R	Y	S	C	P	R	-	-	-	-	-	-	-	-	CD27	
441	R	R	S	S	T	Q	L	R	S	G	A	S	V	T	E	P	V	A	E	E	R	G	L	M	S	Q	P	L	M	E	T	C	H	S	V	G	A	Y	L	CD30		
256	-	-	-	-	-	-	-	-	H	G	C	Q	P	V	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CD40		
222	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4-1BB		
245	-	-	-	-	-	-	-	R	L	P	P	D	-	A	H	K	P	P	G	G	S	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OX40	
308	A	Q	D	Y	E	T	D	T	I	S	Y	R	V	G	N	V	L	D	D	S	H	M	P	G	S	C	N	I	H	K	-	-	-	-	-	-	-	-	-	-	VC22	
311	T	Q	D	Y	E	T	D	T	I	S	Y	H	V	G	N	V	L	D	V	D	S	H	M	P	G	R	C	D	T	H	K	-	-	-	-	-	-	-	-	-	CRMB	
282	-	-	-	-	-	-	-	-	-	-	-	V	A	R	M	P	G	L	E	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6a	
155	-	-	-	-	-	-	-	-	-	-	-	-	G	R	R	C	G	R	G	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6b	

FIG.3M

405	A T W R R R T P R R E A T L E L L G R V L R D M D L L G C - - - - -	-	TNFR1
409	- - - - - D S S P S E S - P K D E - - - Q V P F S K E E C A F - - - - -	-	TNFR2
388	A S W A T Q D S A T L D A - - - - -	-	NGFR
365	- - - - - R G P G D P - P A P P - - - E P P Y P T P E E G A - - - - -	-	LtBr
279	R N W H Q L H G K K E A - Y D T L I K D L K K A N L - - C T L A E K I Q - - - - -	-	FAS
239	- - - - - E E E G S T I - - - - -	-	CD27
481	E S L P L Q D A S P A G G - P S S P R D L P E P R V S T E H T N N K I E K I Y I CD30	-	CD30
263	- - - - -	-	CD40
222	- - - - -	-	Y I 4-1BB
260	- - - - -	-	Ox40
339	- - - - -	-	Vc22
342	- - - - -	-	CRMB
291	- - - - -	-	TNFR-6a
163	- - - - -	-	TNFR-6b

FIG. 3N

[illegible]

FIG. 30

449	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	P A P S L L R	TNFR1
448	P - - - -	- - - - -	- - - - -	L P L G V P D A G M K P S	- - - - -	- - - - -	- - - - -	TNFR2	
413	L V E S L C S E S	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	T A T S P V	NGFR
403	H - - - -	- - - - -	- - - - -	L A E T - E T L G C Q D L	- - - - -	- - - - -	- - - - -	LTbR	
329	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	N E I Q S L V FAS	
247	I Q E D - Y R K P	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	E P A C S P CD27	
560	Y P E Q E T E P P L G S C S D V M L S V E E E G K E D P L P T A A S G K CD30	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CD40	
270	R - - - -	- - - - -	- - - - -	I S V Q - E R Q	- - - - -	- - - - -	- - - - -	G C E L 4-1BB	
236	Q E E D G C - - - - -	S C - - - - -	- - - - -	R F P E E E E G	- - - - -	- - - - -	- - - - -	S T L A K I OX40	
263	I Q E E Q A D A H	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	VC22	
349	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CRMB	
355	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -		
296	F - - - -	- - - - -	- - - - -	L P V - - - - -	- - - - -	- - - - -	- - - - -		TNFR-6a
168	L - - - -	- - - - -	- - - - -	A P - - - - -	- - - - -	- - - - -	- - - - -		TNFR-6b

FIG. 3P

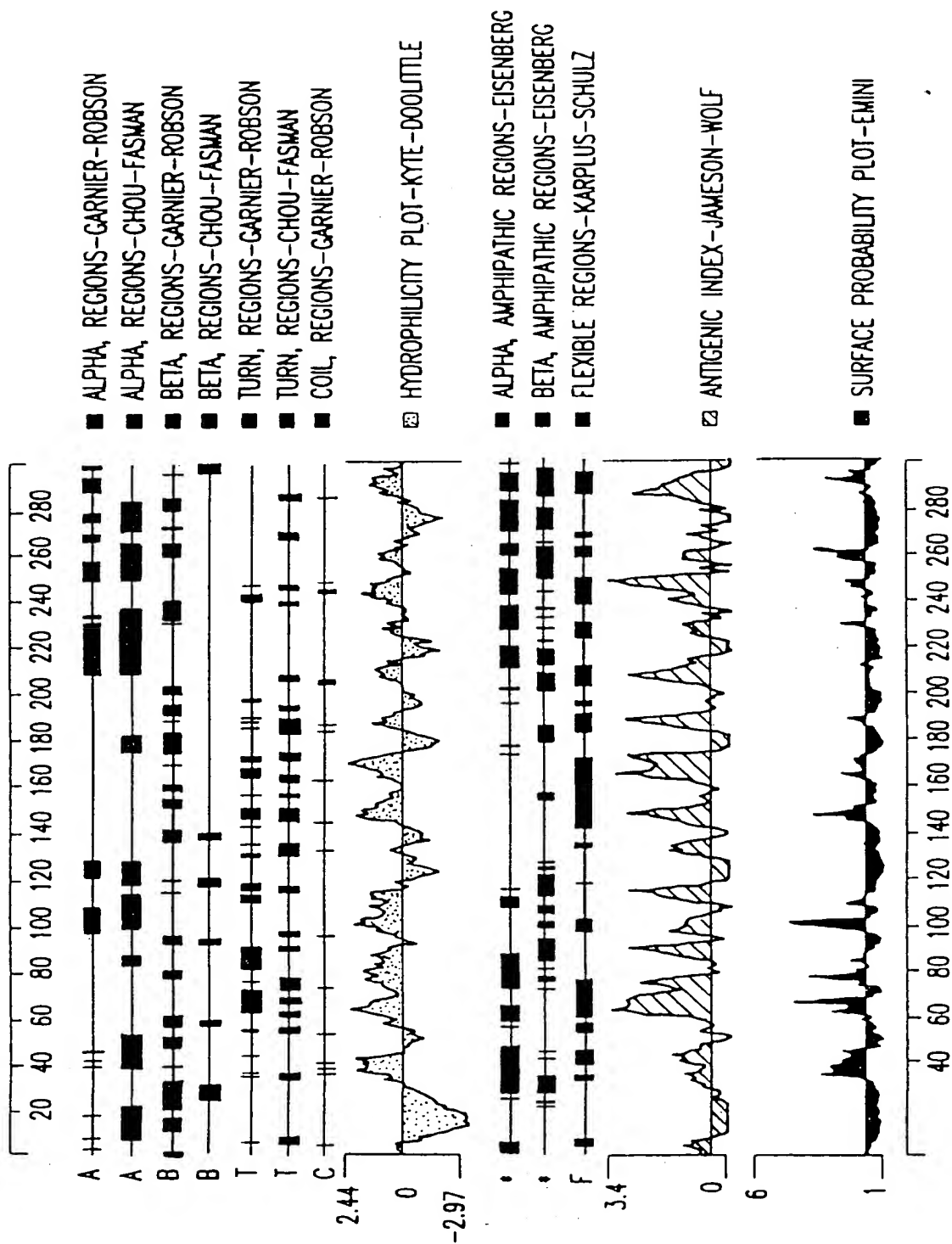
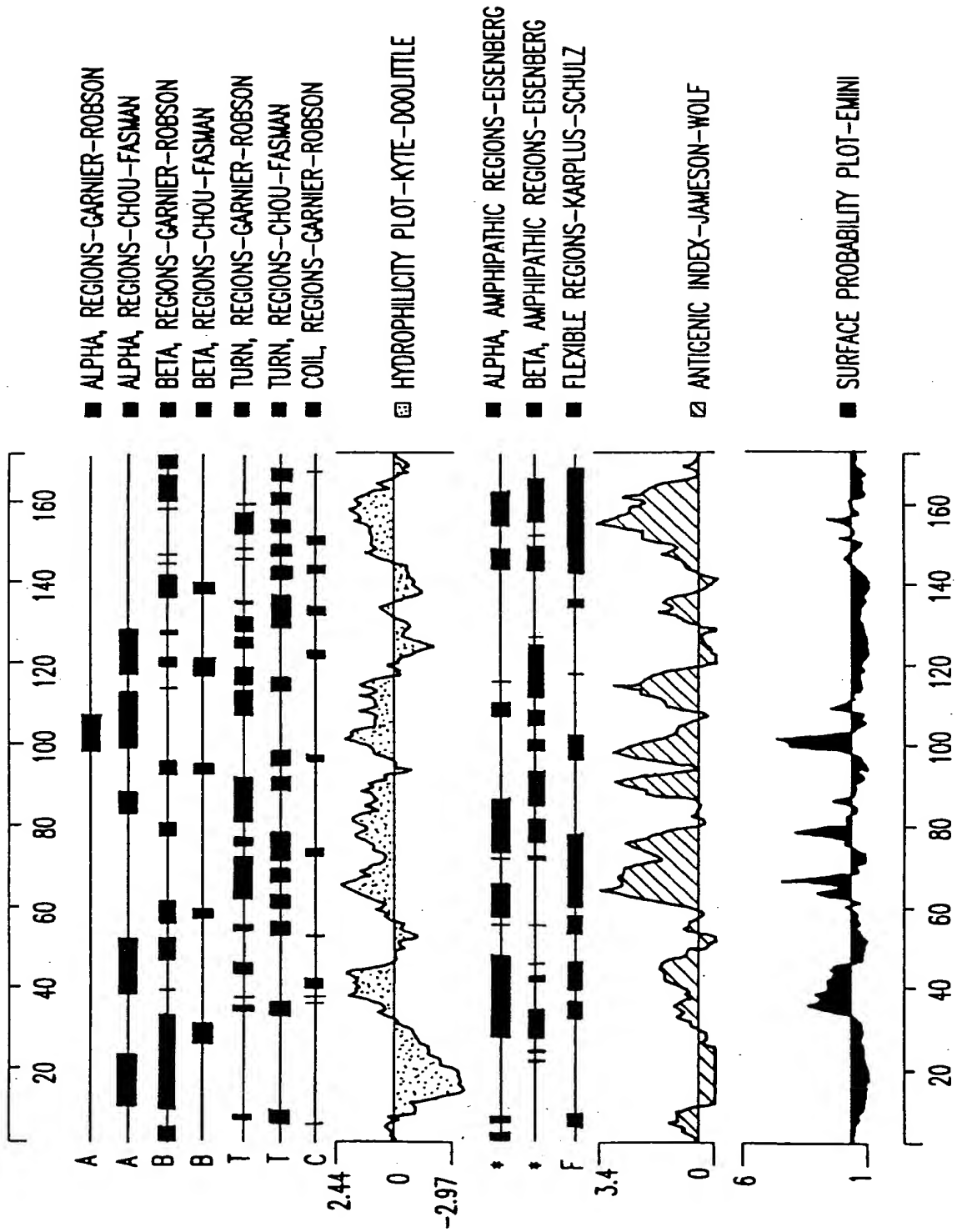


FIG.4



22/23

HELDI06R

GGCACGAGCA GGGTCCTGTN TCCGCCCTGA GCCGCGCTCT NCCTGCTCCA GCAAGGACCA
TGAGGGCGCT GGAGGGGCCA GGCCTGTGCG TGCTGTGCCT GGTGTTGGCG CTGCCTGCCC
TGCTGCCGGT GCCGGCTGTA CGCGGAGTGG CAGAAACACN NACNTACCCC TGGCGGGACG
NAGAGACAGG GGAGCGGCTG GTGTNTNCCC ANTGCCCCC AGGCACCTTT NTGCAGCGGC
CGTGCCGNCG AGACAGCCCC ACGACGTGTG GCCCGTNTCC ACCGCGCCAC TACACGCATT
CTGGA ACTAC CTGGAGCGCT GNCGTTACTN CAACGTCCTC TCGGGGAGC GTNAGGAGGA
GGCACGGGTT TNCCACGNCA ACCACAACCG NGGNTTACCG TNGCCGNACC GGTTTCTTCG
NKGCAAGTTG GTTTTTNNTT TGGAGNAAGG ATTCGTGTIN CAATTNATTG ACGNAGTGAT
TNNNCNCGGG AAAC TNAAA

HCEOW38R

CGCAACTGCA CGGCCCTGGG ACTGGCCCTC AATGTGCCAG GNTCTTCCTC CCATGACACC
CTGTGCACCA GCTGCACTGG CTTCCCCCTC AGCACCAGGG TACCANGAGC TGAGGAGTGT
GAGCNTGCCG TCATCGACTT TTTGGCTTTC CAGGACATCT CCATCAAGAG GCTGCAGCGG
CTGCTCANGC C

FIG.6

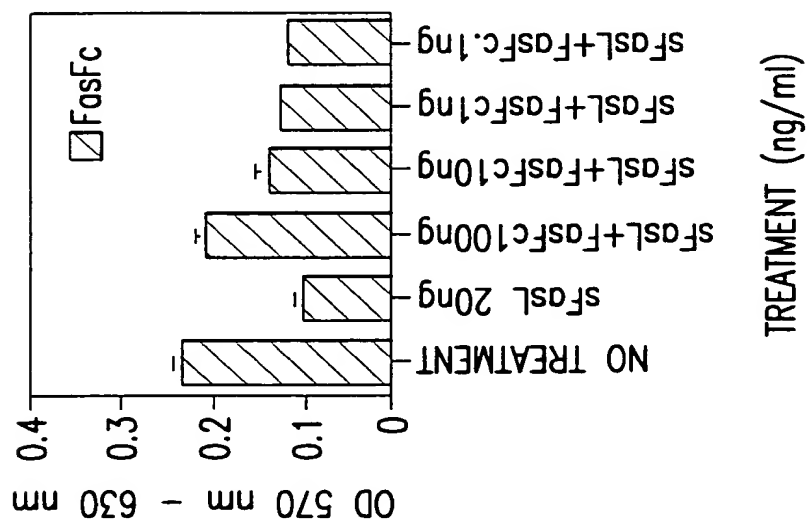


FIG. 7A

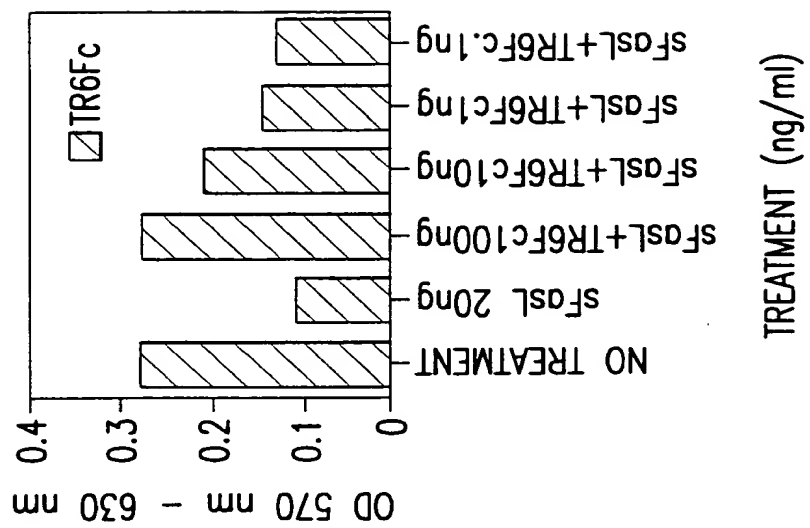


FIG. 7B